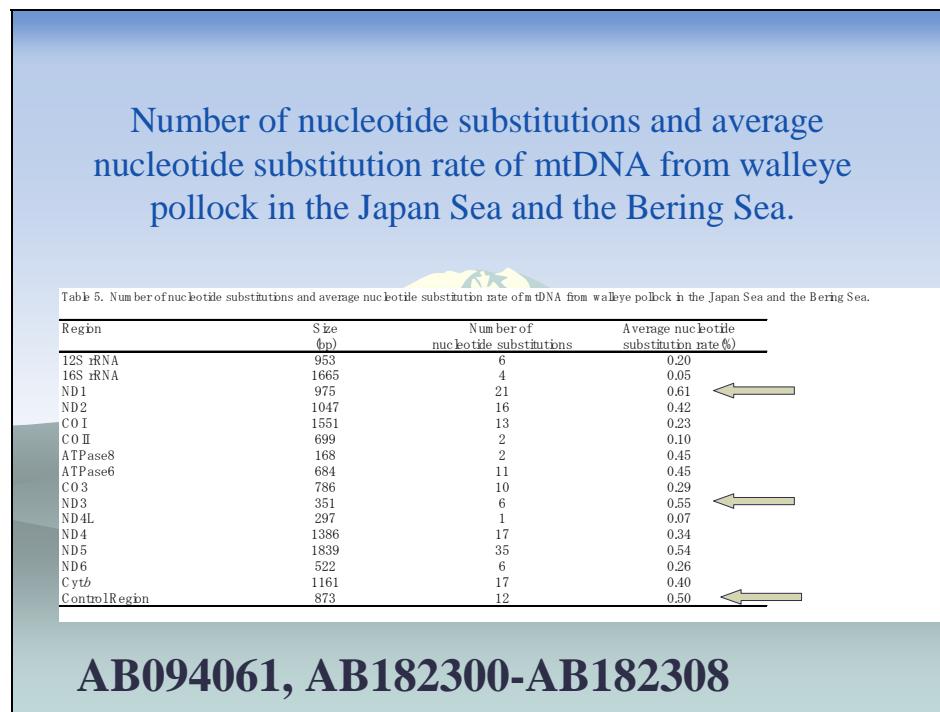
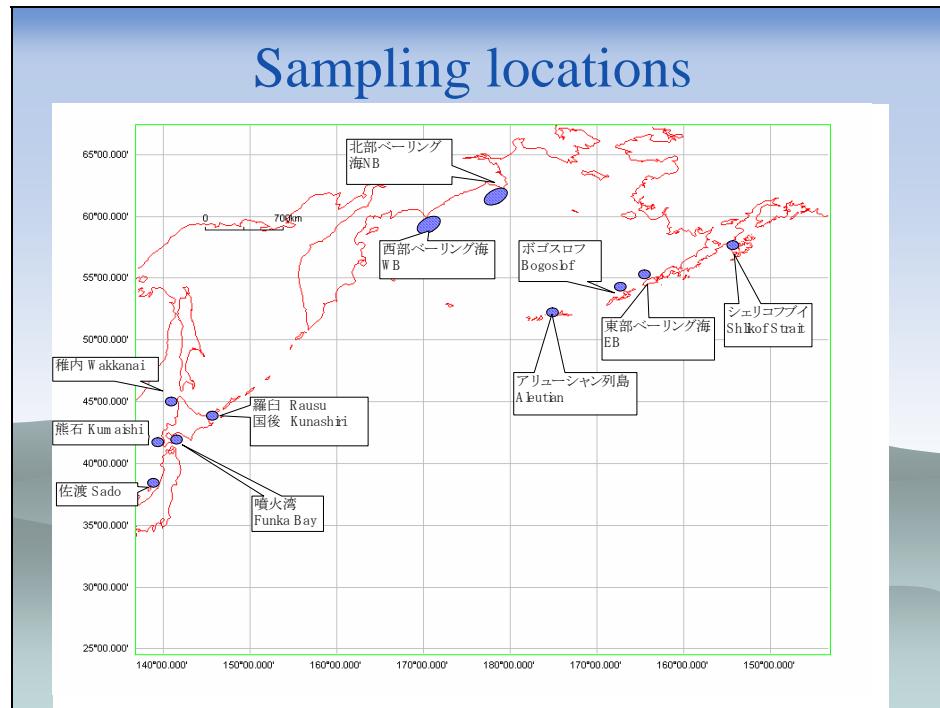


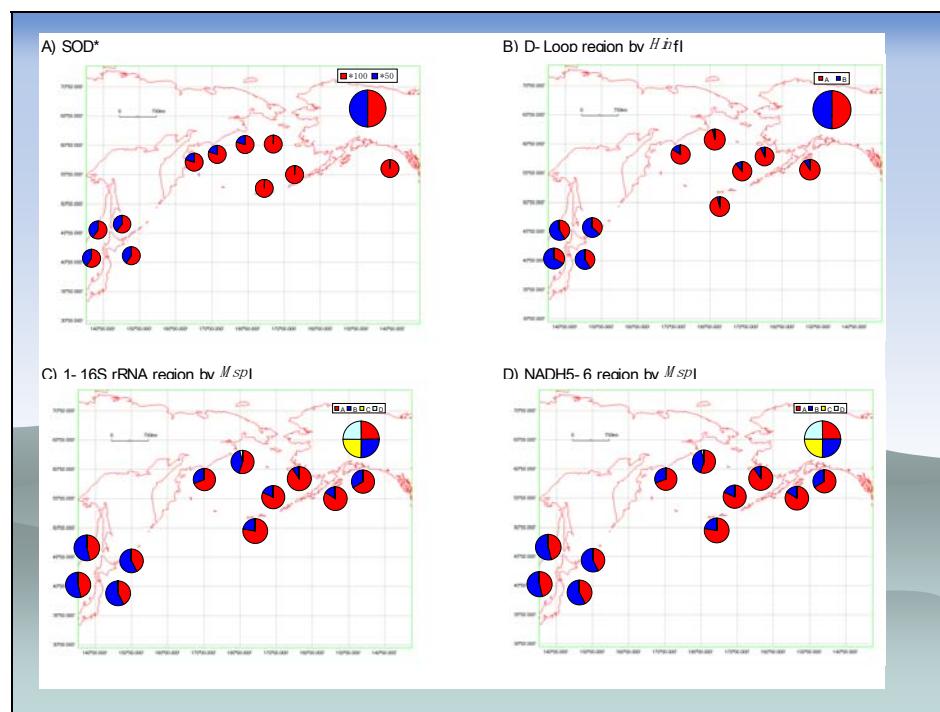
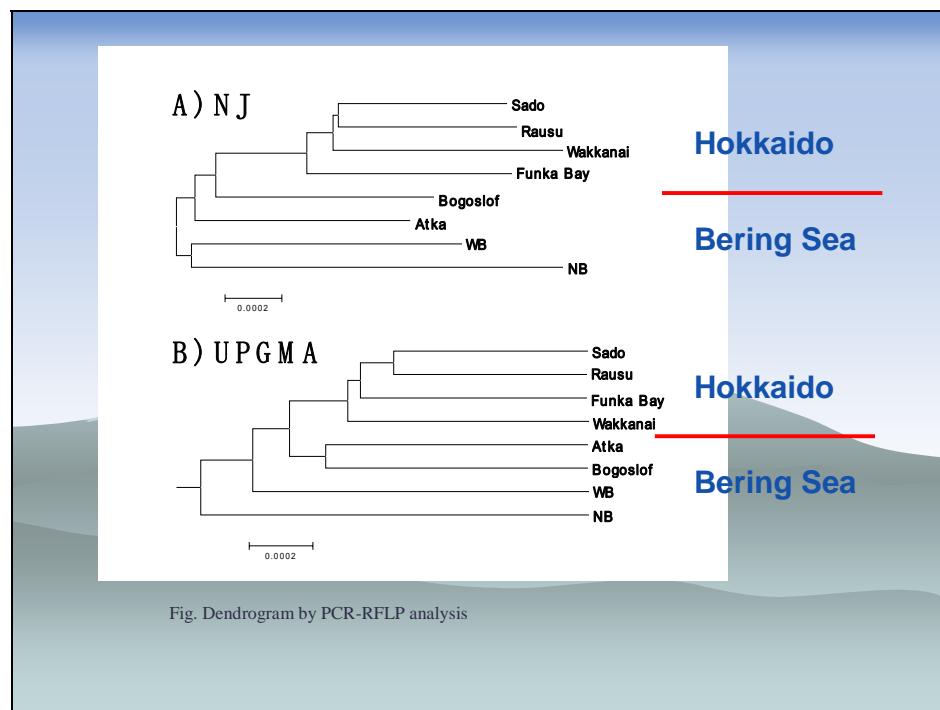
Summary of DNA analysis of walleye pollock by Japanese Scientists (2005)

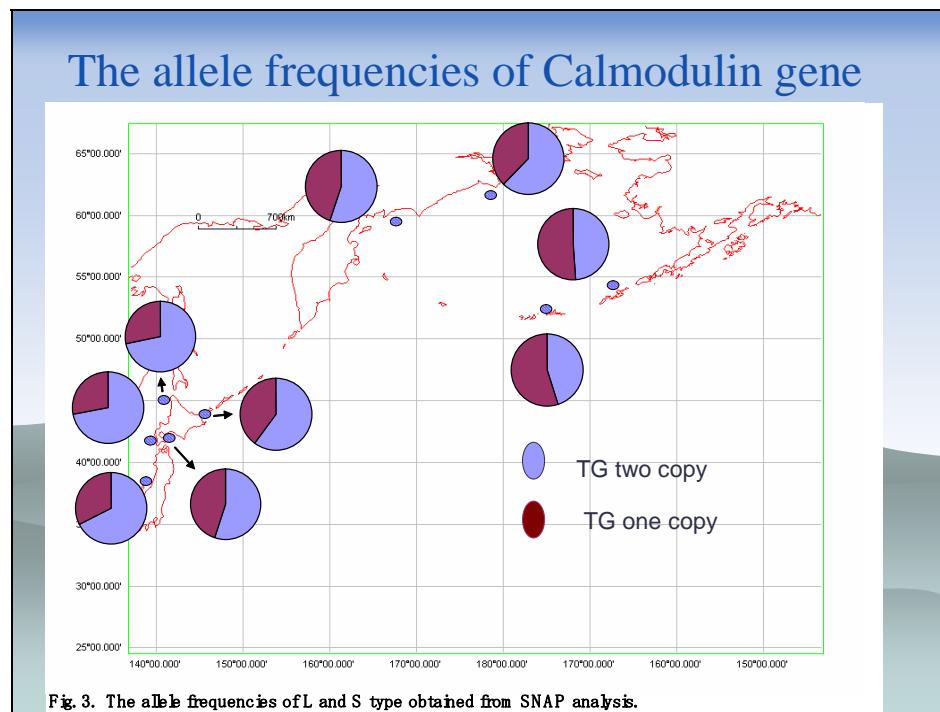
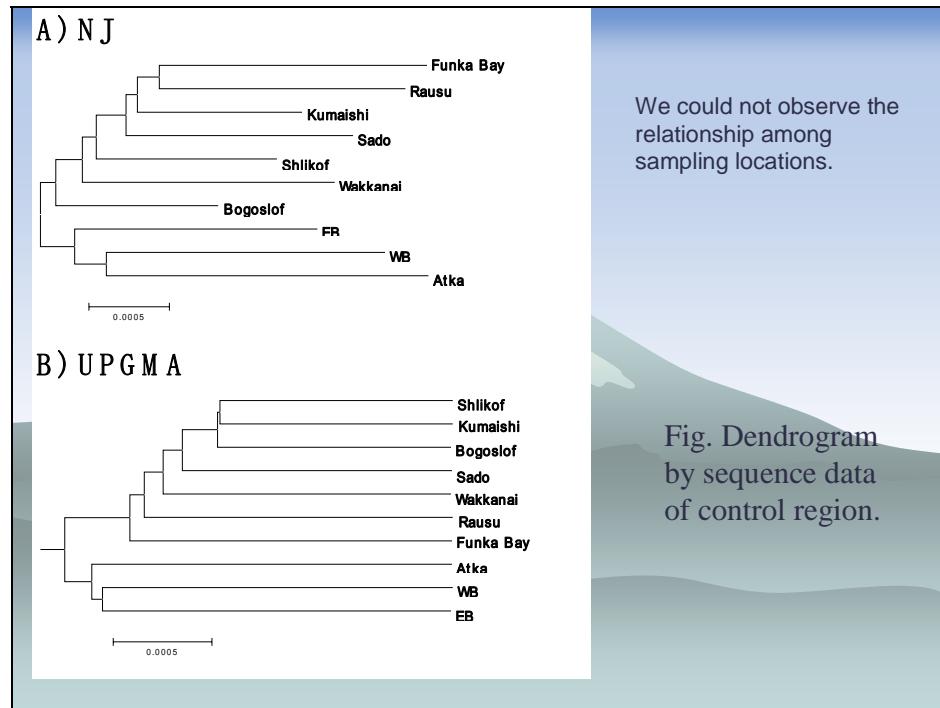
- ◆ Takashi Yanagimoto (FRA, HNF)
- ◆ Toru Kitamura (Japan NUS co. jp)
- ◆ Takanori Kobayashi (FRA,NRIFS)
- ◆ Ichiro Nakayama (FRA,NRIFS)

DNA analysis

- ◆ Total mtDNA Sequenced
- ◆ mtDNA PCR-RFLP analysis
- ◆ mtDNA control region sequenced
- ◆ Nuclear DNA analysis (RAPD, TREP, SNP analysis of Calmodulin gene)







Dendrogram of relationships among sampling areas using SNAP data

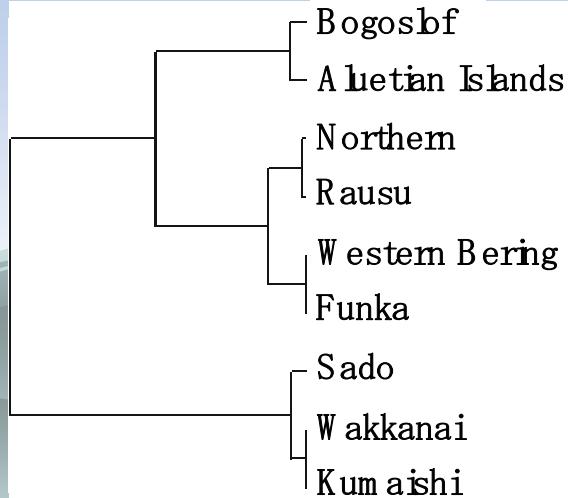


Fig. 4. UPGMA dendrogram of relationships among sampling area of walleye pollock.

Population structure

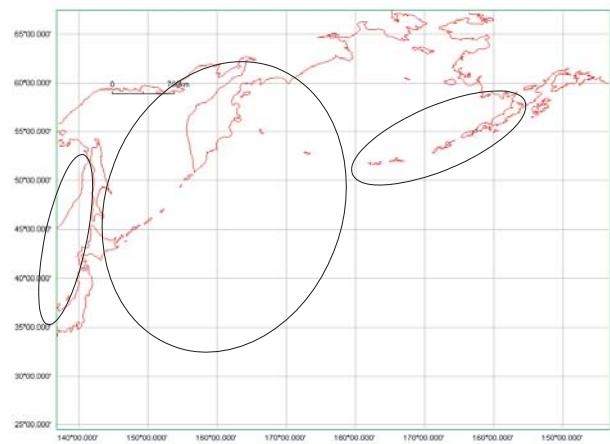


Fig. 5. Population structure of walleye pollock from this study.

Summary

- ◆ There were no area-specific nucleotide variations among sequences of mtDNA control region.
- ◆ In NJ tree, groups were formed without relations of the sampling locations by sequences data.
- ◆ In RFLP analyses, there were no area-specific fragment patterns. But the distribution of fragment patterns from three regions showed differences among sample sites.
- ◆ Composite mtDNA haplotype frequencies were different between Western Pacific and Bering Sea.
- ◆ Based upon SNAP analysis of Calmodulin region, these results are similar to past results (Allozyme).